

RESU

JLT 5

QY 2521 TTCCCGTGGCCACTTGCCCCGAAATGTCAGCAGCAGCCCTCGTGGCAGAGG 2580
 Db 862 LeuArgLeuAspAsnValGly-----GluaLargSerProGlnAspArgSer 877
 QY :::::|||:
 Db 2581 GGCCmCTCTCACT-----GTTCCCCATGGGCCAGGGCA 2616
 QY :::::|||:
 Db 878 ProIleLeuAlaLysHisSerPhySerProIleLeuGluLysValAla 897
 QY :::::|||:
 Db 2617 AGGAACACAGACACACTGGACAAGGCTTGCSCAGGGTGACAGACTGTTAGAGAGG 2676
 QY :::::|||:
 Db 898 ThrValLeuGluValAlaLysHisGluLeuLysGluAspIleLeuAsnAla 917
 QY :::::|||:
 Db 2677 CTGCACTGCGGAGAGACTCAGTCAGTGGCTGCGCAGCTTGRCCTGGCCC 2736
 QY :::::|||:
 Db 918 ThrSerIleGlyLysInLeuSerGluIleLeuArgIleLeuMet----- 932
 QY :::::|||:
 Db 2737 CACAGGAGGGmCCTGCCCTGGGAGTGGCTGCGCAGGCCAGCACCTCC 2796
 QY :::::|||:
 Db 933 -----SerArgGlySerSerGlnSerIleGlnAspThrCys 944
 QY :::::|||:
 Db 2797 GAGCTCTGCAGCT 2811
 QY :::::|||:
 Db 945 GluValSerArgPro 949

Result 8
 I8912 potassium channel subunit - mouse
 C;Species: Mus musculus (house mouse)
 C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 05-Nov-1999
 C;Accession: I48912
 R;Wormke, J W ; Ganetzky, B
 Proc. Natl. Acad. Sci. U.S.A. 91, 3438-3442, 1994
 A;Title: A family of potassium channel genes related to eag in Drosophila and mammals.
 A;Reference number: A54953; NID:94211879; PMID:8159766
 A;Accession: I48912
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: mRNA
 A;Residues: 1989 <RES>
 A;Cross-references: EMBL:U04294; NID:9487739; PIDN:AAA62474.1; PID:9487740
 C;Genetics:
 C;Gene: m-eag

Alignment Scores:
 Pred. No.: 1.16e-63 Length: 989
 Score: 1371.50 Matches: 341
 Percent Similarity: 50.14% Conservative: 189
 Best Local Similarity: 32.26% Mismatches: 310
 Query Match: 22.52% Index: 217
 DB: Gaps: 31

US-09-965-830-1_COPY_6_3257 (1-3252) x 148912 (1-989)

QY 13 CGGGGCTCCmGCCCCCTCAGAACCTTCTGGACACCATCGCTACGGCCTCCAGGC 72
 Db 8 ArgGlyLeuValAlaProGlnAsnAlaThrPheLeuGluAsnIleValArgArgSerAsnAsp 27
 QY :::::|||:
 Db 73 AGCCACAGTAACCTGCTGGCCAGGCCAGGmGCGCTTCCTCCGGTCTAC 132
 QY :::::|||:
 Db 28 Thr----AsnPheValLeuGlyAsnAlaGlnIleValAsp--TirProIleValTyr 44
 QY :::::|||:
 Db 133 TGCTCTGATGGCTCTGTGACCTCACGGCTCTCCGGGTGAGCTCAGCAGGGGG 192
 QY :::::|||:
 Db 45 SerAsnAspGlyPheCysIleLeuSerGlyTyrIleArgAlaLysValAla 64
 QY :::::|||:
 Db 193 TCTGCCGCTCTTCCCTTGGCCAGACACCTGAGCTGCTGCCAACAGATCCG 252
 QY :::::|||:
 Db 65 SerAlaAspSerPhyMattyArgYGLuLeuThrAspLysAspThrValGlyLysValArg 84
 QY :::::|||:
 Db 253 AAGGCCCTGGAGCACAGGAGTCAGGCTGAGCTGCTACCGGAGAsGGG 312
 QY :::::|||:
 Db 85 GlnThrPheGluAsnTyrGluLeuThrAspSerPheGluLeuMetTyrLysAsnArg 104
 QY :::::|||:
 313 CTCGGTCTGGTCCTGGATGTATACCCATAAGATGAGAAGGGGGGGCT 372

Db 105 ThrProValTirPhePheValLysIleAlaProIleArgAsnGluLysVal 124
 QY :::::|||:
 Db 373 CTCTCTCTAGCTCTCTCACAAAGGACTCAGGAAACCAAGAACGAGGGGGCCACAGA 432
 QY :::::|||:
 Db 125 LeuPheLeuCysTyrThrPheSerAspLeuAspIleThrAlaPheLysGlnProIleGluAspAsp 144
 QY :::::|||:
 Db 433 TGAAGGAGACAGGmGCTGGCCC-----CGCCGATATGGCCGGCACGATGCAAAAGCTC 489
 QY :::::|||:
 Db 145 CysLys-----GlyTyrPheAlaArgLeuThrArgAlaLeuThr----- 160
 QY :::::|||:
 Db 490 AATGCCAACCGGGCGGAGGGGGCGTCTACACCTGTCGGCACCTGAGAG 549
 QY :::::|||:
 Db 161 -----SerArgGlyValLeuGlnIleLeuAlaSerAlaSerValGlnLys 174
 QY :::::|||:
 Db 550 --CAGCCCAAGGGCAGCAC-----AAGCTCAAAAGGGGG 585
 QY :::::|||:
 Db 175 GlyLysAsnValAlaLysHisSerArgIleAlaLysValLeuGlySerAspIle 194
 QY :::::|||:
 Db 586 TmGGGGAAACCAAACTGCTGAGTACAAGTAGCCGCACTCCGAAAGGGCTTC 645
 QY :::::|||:
 Db 195 -----LeuProGlnTyryLysIleIleAlaProIleThrProProHis 208
 QY :::::|||:
 Db 209 IleIleLeuHisTyrCysValPheLysIleIleLeuIleLeuThr 228
 QY :::::|||:
 Db 706 CTCTATGTTGCTGCACTGTGCTTACAGCTGCTGAGCACAGCACGGGAGCCAGT 765
 QY :::::|||:
 Db 229 PheTyrThrAlaIleLeuValProTyryAsnAlaSerPheLysThr--ArgInAsnAsn 247
 QY :::::|||:
 Db 766 GCCCCCAGGGCCGCCCCAGGCTGTGAGCTGCGCTGGAGGTCTCTCACCTGAC 825
 QY :::::|||:
 Db 248 ValAlaTrp-----LeuValValAspSerIleValAspValIlePheLeuValAsp 264
 QY :::::|||:
 Db 826 ATGGTGCCTGATTCGTAACCACTTCGCTGCTGAGCTGGGCAAGGTGCTGTTGCCCA 885
 QY :::::|||:
 Db 265 IleValLeuAsnPheHistThrThrPheValGlyProAlaGlyIleValLeuSerAspPro 284
 QY :::::|||:
 Db 886 AGTCATTCGCTTCCACTAGTCACCACTGGTCCTGCTGGATCTCGCAGGGCTG 945
 QY :::::|||:
 Db 285 LysLeuIleLeuGlyMetAsnTyryLeuLysIleValAspLeuIleLeuSerCys 304
 QY :::::|||:
 Db 946 CCCTTGACCTGCTACATGCTTC-----AAGGTCACGTGTTACTGGG-- 990
 QY :::::|||:
 Db 305 ProTyPheAspValIleAsnAlaPheGluAsnValAspGluValSerAlaPheMetGlyAsp 324
 QY :::::|||:
 Db 990 -----

Db 325 ProGlyLysIleGlyPheAlaAspGlnIleProProIleLeuGluIleLeuGlyArgGluSerGln 344
 QY :::::|||:
 Db 991 -----GCCCATCTGCTGAAGGGGmGCGCTGCGCCmGCTGGCCCTG 1035
 QY :::::|||:
 Db 345 GlyIleSerSerIleLeuPheSerSerIleIleLysValAlaArgLeuIleLeuGlyArgVal 364
 QY :::::|||:
 Db 1036 CmTCCGGGCTGAGCCGTAATCGCGACTACGCGCTGCGCTGCGCTGACACTGCTCAmGCC 1095
 QY :::::|||:
 Db 365 AlaArgLysLeuAspHisTyrIleGluTyryIleAlaIleLeuIleLeuValAlaCys 384
 QY :::::|||:
 Db 1096 GmTCCGGGCTGAGCCGTAATCGCGACTACGCGCTGCGCTGCGCTGACACTGCTCAmGCC 1155
 QY :::::|||:
 Db 385 ValPheGlyLeuAlaAlaHistPheMetAlaCysIleIlePheSerIleGlyAspTyrGlu 404
 QY :::::|||:
 Db 1156 ATGGAGACGCAATCCGAG--CmGCTGAGATGCTGCTGCTGAGGACCTGGCCG 1212
 QY :::::|||:
 Db 405 IlePheAspGluAspPheThrIleArgAsnAsnSerTirPheLeuIleLeu 424
 QY :::::|||:
 Db 1213 CGCTGGGACTCTACCTACmGGTGGCCGGAGGCCAGCTGAGGGACACCTGGG 1272
 QY :::::|||:
 Db 425 AspIleGlyLysThrProTyryGlnPhe-----AsnGlySerGlySerGly 438
 QY :::::|||:
 Db 1273 CAGAGCACACTCCAGGAGCAGGCCAACGGGAGCAGGGCTGAGGCTGCTGGC 1332

QY	1	ATGCCG--GCCATGGGGGCTCTGGGCCCTAGAACCTTCTGGCACCATCGCT
Db	1	MetProAlaGlyIysAsnGlyLeuValAlaProIleAsnThrPheLeuGuaValle 20
QY	58	ACGGCTTGCACGCCACGACTGCTGCTGGGAAACGCCACGGCTCTGGCT 117
Db	21	ArgArgcysAsnAsnAlaAspThrSerPheIleLeuAlaAsnAlaGlnValAla 39
QY	118	TCGCCGGGCTACTGCTCTGAGGGCTCTGACTCACGGCTCTCCGGGCTGAG 177
Db	40	TyrProIleValTyrCysAsnAspAlaPheSerLysLeuValGlyTyrThrArgAla 59
QY	178	GTCAGCAGGGGCTGCTGCTCTGCTTATGGCCAGAACCAAGGAGCTGTC 237
Db	60	IleMetGlnIysProCysSerLeuAlaPheMetHisGlyIysGlyLvaValGly 79
QY	238	CGCCAAAGATCCCAAGGCTCTGGACGAGCACAGGTCAGGTCAGGCTGATCTG 297
Db	80	LeuGlnIlysMetGlnIleAlaIleLeuGuaAsnAlaArgThrGluGlnAlaGluIle 99
QY	298	TACCGAGGAGGGCTCCCTCTGGTCCTCTGATGATGATACCCATAAGATGAG 357
Db	10	CysLysIlysAsnLysThrProIlePheLeuValHisLeuAlaProIleLysAsnHis 119
QY	358	AAAGGGAGGAGGGCTCTTCCTAGTCCTCACAAAGGATCACGGCATCGCAGAACCGA 417
Db	120	LysAspIleAlaValValLeuTyroIleCysGlnPheLysAspIleThrProIle 139
QY	418	GGGGCCCCGACAGATGGAGGAG-----AcAGGTTGGCCGGCCGATAT 465
Db	140	LeuAspAspGluAsnAsnLysAlaLeuPheCysValThrGlyLysAla----- 155
QY	466	GCCGGGGGACGATCCAAAGGCTCATGCCAACCGCCGAGCCGGCCGCGCTCTAC 525
Db	156	-----AsnIleAlaValGluLysValThrArgAlaValMet----- 166
QY	526	CACCTGTCGGGCACCTCGAGAAGCAGGCCAACGGCAAGCACAAAGCTCATAGGGTG 585
Db	167	AsnIleUgiGlyIysAspMet----- 172
QY	586	TTGGGGAAACCAAACTGCTCTAGTCAAAGTAGGCCCATCCGGAAATGCCCTTC 645
Db	173	-----LeuProGlnItyArgGlnGluThrProIleThrSerProHis 186
QY	646	ATCTGTGTCACGTGGGCACTGAGGCCACCGAGGATGCCCTCCCTGCCACA 705
Db	187	IleIleLeuHistItySerSerPheIleLeuIlePheIleLeuThr 206
QY	706	CTCTATGTCGTGACTGCCCTACAGCGTGTGAGCACGCCAACGGAGCCAGT 765
Db	207	PhenylAlaPheMetValProPheAsnIleAlaPheLysAsnSerSerSerArgGluAsn 226
QY	766	GCCGCCGCGGCCGCCACGGCTCT-----GACCTGGCGTGGGGCTCTCATC 819
Db	247	AlaAspIleLeuAsnPheHistIleThrPheValGlyProGlyIysGluValle 266
QY	820	GCCCAAAGTCATTGCCCTACTAGTCACCCAGGGTTCTGGATGTCATCCA 939
Db	267	GluProSerValIleArgGlnAsnTyPheIysSerTrPheIleLeuAspLeuSer 286
QY	940	GGCTGGGCCATCTGCTGAGACGGTGCCTCTGCTGCCCTGCTGCCCTGCTGCCGG 1044
Db	307	CysLeuIroTyAspIlePheItyMetPheLysArgAspAspGluArgIleGlySerLeu 324
QY	1045	CTGGACCGGACTCGCACTACAGGCCGCGTGTGACACTGCTGACAGGGTGTGCC 1104

Db	325	LeuAspAsnTyrIleuGluGlyAlaAlaThrIleuLeuLeuLeuCysAlaTyrVal	344
QY	1105	CTGCTCGGCCACTGGTGCCTCTGGCTCTGGTTACATGGCCAGGGGGAGTC-----	1158
Db	345	IleValAlaHisIlePheLeuAlaCysValIlePheIlePheIlePheIlePheIle	364
QY	1159	GAGCCAGGAACTCCGACCTGAGATGTCGCTGAGAGCTGGCTGGCTGAGAGCTGGCCCGGACTG	1218
Db	365	LysMetAspAsnLeuAlaLeuProAsp---GlyIlePheIlePheIlePheIlePheIle	383
QY	1219	GAGACTCCCTACTACTCTGGGGGGAGGCCACCTGGAGGGACAGCTCCGGCAGAGT	1278
Db	384	ArgIleHisTyr-----	387
QY	1279	GACAATGCGACGCCAGCAGCAGCAGGAGGAGGGGGCTGGAGCTGCTGGCCGCC	1338
Db	388	---AspIleProLeuSerAsnIleIlePheIlePheIlePheIlePheIlePheIle	401
QY	1339	TGCTGCGCACGCCCTACATGACCTCCCTACTTGCACATCAGCAGCCTACCCGCGTGT	1398
Db	402	SerArgThrSerAlaTyrIleSerSerLeuIleGlyThrIleSerCysMetSerThrVal	421
QY	1399	GGCTTCGGCAGCTGTCGCCACAGGACAGGAGAGAGCTCTCCACAGCAGCTG	1458
Db	422	GlyPheGlyAsnIleAlaSerAsnIleAsnIlePheGlyIlePheGlyIlePheGlyIle	441
QY	1459	CTCATCGGCCGCTGTATGCCACCGGGTGTGTTGGGACCTGACGCCATCATCCAGCGC	1518
Db	442	IleIleSerAlaIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIle	461
QY	1519	ATGTAACGCCGCCGCTTCTGTACACAGCCACGGGGACCTGGCCACTACATCGC	1578
Db	462	MetThrSerSerThrValArgTyrIleIleGlyIleIleGlyIleIleGlyIleIle	481
QY	1579	ATCCACCGTATCCCCAACCCCCCTAACAGGCCATGCCGAGGACTTCAGGCCACCTG	1638
Db	482	LeuIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIle	501
QY	1639	GCCTGTGAACTAACATGCCATCACACCCGCTGCTGCCAGGCCCTCCCTGACAGCTGCC	1698
Db	502	AlaMetThrIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIle	521
QY	1699	GCAGACATGCCATGCCACCTGCAAGGGGCTCTG---CAGCTGCCACTGTTGAGGGG	1755
Db	522	AlaAspIleCysValIleHisIleAsnArgIleValPheAsnIleGluIleIleIle	541
QY	1756	GCCACGCCGCTGCTGCCGCGACTGTCCTGGCCCTGGCCGCCCTCTGCCAGCGC	1815
Db	542	AlaSerAspIleCysIleLeuSerAlaMetPheIleIleIleIleIleIleIleIle	561
QY	1816	GGCAGACTCCATCCACCAAGGGATGCCCTGCAAGCCCTACTTGTCTGCTCTGGC	1875
Db	562	GlyAspIleLeuIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIle	581
QY	1876	TCCATGAGGCTCTGAGGGTGCACGCTGCTGCCATCTTGGAGGGAGGCCGACCTG	1935
Db	582	SerLeuIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIle	601
QY	1936	GGCTGTGAGCTCCCCGGGGAGCAAGGGTAAGGCCAAT-----	1977
Db	602	Gly-----AspIlePheIlePheIlePheIleAsnGlySerIleGlyIleGlyIle	615
QY	.1978	--GCCGAGGCTGAGGGCCCTGACTACTGGCTCTGCACGCTGCTGCTGCTG	2034
Db	616	AlaAlaLysValArgAlaIleIleIleIleIleIleIleIleIleIleIleIleIle	635
QY	2035	CAAGCACACCTGGCTGCTACCCGAGTTGGCTGGCCCTGAGCTGGCTCCGG	2094
Db	636	MetAspValIleAspPheIleIleIleIleIleIleIleIleIleIleIleIleIle	653
QY	2095	GAGCTCACTACACCTGGCTGGGGAGGCCAGAGCTGGGACACAGCTCCCTG	2154

Us-09-965-830-1_copy_6 3257.rpt

Db	270	ProTyr-----		
Qy	1285	TCCAGCAGCAGCAGGGGACACGGGACGGGGCTGGAGGTGCTGGGGGGCGCGTG	1344	
Db	272	-----ThrSerThrAsnGlyThr-----IleProThrGlyIyProThrIeu	285	
Qy	1345	GGAGGCCATCACCTCTACTTGCACAGCAGCTCAGCAGCCTCACACGGGCTC	1404	
Db	286	LyserArgSerValThrAsnValSerAlaIleGlnArgLeuSerIleThrSerIleGly	305	
Qy	1405	GCGAACGCTGCGCCACACGGACACGGAGATCTCCTCCATCGCACATGCTCATC	1464	
Db	306	GlyAsnValSerAlaIleThrAspSerGlyIeuIleSerIleThrIleMetIleu	325	
Qy	1465	GGGCCCTGATGACGGGTTGTTGAAAGTGACGGCATCAGCGCAGTCACATCGC	1524	
Db	326	GlySerIleMetTyrIleAspSerValIleProGlyIeuValSerAlaIleGly	345	
Qy	1525	GCGGCCGCTTGACGACGGGACGCCGACTCTGGGACTACATCGCACAC	1584	
Db	346	SerGlyIleAlaArgGlyIleIleGlyIeuValSerAlaIleGlyIeuArgLeu	365	
Qy	1585	CGATCCCCAACGCCCTAACAGAGCGCAGTCAGACTTCAGGCCACCTGGCGTG	1644	
Db	365	GlnIleProAsnProLeuIleArgGlyIeuArgIleGluIleGlyIeuIle	385	
Qy	1645	AACATGGATGACGCCACCGAGCTGTCAGCCCTCGACGAGCTGGCGCAGAC	1704	
Db	386	ThrAsnGlyIleAspMetIleValLeuIleGlyIeuAspIleAspIleGly	405	
Qy	1705	ATCGCCATCACCTGCACAGGAGGTGCGAG--CTGCCACTGTTGAGGGCCAGC	1761	
Db	406	IleCysIleIleIleAsnAlaGlyIleLeuSerIleGlyIeuAlaIleGly	425	
Qy	1762	CGCGGTGCCGCGGGCACTCTCTGGCTCTGGCCCTGGCGCCCTCTGCACGGCG	1821	
Db	426	ProGlyCysLeuValGlyAlaLeuSerMetArgPheArgThrThrHisSer	445	
Qy	1822	TACCTCATCCACAGGGGAGGCCCTGAGGCCCTACTTGTGCTGCTGGCTCAG	1881	
Db	446	ThrLeuValIleIleAspGlyAspIleLeuIleArgGlyIeuValIleGly	465	
Qy	1882	GAGGTCTCAG---GGTGCACCGGCTGCGCACCTCTGGAAAGGGCCACCTGATGCG	1938	
Db	466	GlutLeuIleAsnAspAspAsnThrValMetGlyIleIleGlyIeuAspIle	485	
Qy	1939	TGAGGAGCTGCCCGGGAGGAGGTGGTAAGGCCAAATGCCGACGTGAGGGCTGAGC	1998	
Db	486	GluAsnProLeuIleIleAspGluValGlyIeuSerSerCysAsnValArgAla	505	
Qy	1999	TACTGGCTCTG 2010		
Db	506	TyCysAspIeu 509		
RESULT	11			
A55251				
C;Species: Bos Przewalski taurinus (cattle)				
C;Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 13-Aug-1999				
C;Accession: A55251; 543976				
R;Biel, M.; Zong, X.; Distler, M.; Bosse, E.; Klugbauer, N.; Murakami, M.; Flockerzi, V.				
Proc. Natl. Acad. Sci. U.S.A. 91, 3505-3509, 1994				
A;Title: Another member of the cyclic nucleotide-gated channel family, expressed in test				
A;Reference number: A55251; MUID:94224768; PMID:8170936				
A;Accession: A55251				
A;Status: nucleic acid sequence not shown				
A;Molecule type: mRNA				
A;Residues: 1-706 A				
A;Cross-references: GB:X76485; NID:9488728; PID:CAA54023.1; PID:9488729				
A;Experimental source: kidney				
R;Weyand, I.; Godde, M.; Frings, S.; Weiner, J.; Mueller, F.; Altenhofen, W.; Hatt, H.				
Nature 368, 859-863, 1994				
A;Title: Cloning and functional expression of a cyclic-nucleotide-gated channel from man				

A: Reference number: S43976; MUID:94211295; PMID:7512693
 A: Accession: S43976
 A: Status: preliminary; nucleic acid sequence not shown
 A: Molecule type: mRNA
 A: Residues: 1-706 <WET>
 A: Cross-references: GB:x89500; NID:9908823; PIDN:CAA61759.1; PID:9908824
 A: Experimental source: testis
 C: Genetics:
 C: Gene: CNG3
 C: Superfamily: cyclic nucleotide-gated channel; cAMP receptor protein cyclic nucleotides;
 C: Keywords: cGMP binding; ion channel; ion transport; membrane protein
 C: Domain: cAMP receptor protein cyclic nucleotide-binding domain homology <CA_501-625>

Alignment: Scores:	2.25e-15	Length:	706
Pred. No.:	439.00	Matches:	145
Score:	42.5%	Conservative:	101
Percent Similarity:	25.0%	Mismatches:	208
Best Local Similarity:	7.21%	Indels:	124
Query Match:	2	Gaps:	19
DB:			

US-09-965-830-1_COPY_6_3257 (1-3252) x A55251 (1-706)

Db 608 aAsnIleArgSerIleGlyTyrSerAspLeuPheCysLeuSerLysAspAspSpleuMetG 628
OY 2040 CAGCCCTTGCCGCTGTAACCCCGAG 2061
Db 628 uAlaLeuThrGluTyrProGlu 635

RESULT 13
552072
DmCNC protein - fruit fly (*Drosophila* sp.)
C;Species: *Drosophila* sp.
C;Date: 14-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 16-Jul-1999
C;Accession: S52072
R;Baumann, A.; Frings, S.; Godde, M.; Seiffert, R.; Kaupp, U.B.
EMBO J 13, 5040-5050, 1994
A;Title: Primary structure and functional expression of a *Drosophila* cyclic nucleotide
A;Reference number: S52072; MUID:95045396; PMID:7957070
A;Accession: S52072
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-665 <BAU>
C;Genetics:
A;Gene: FlyBase:Cng
A;Cross-references: FlyBase:FBgn0014462
C;Superfamily: cyclic nucleotide-gated channel; cAMP receptor protein cyclic nucleotid
C;Domain: 550-555 domain; cAMP receptor protein cyclic nucleotide-binding domain homology <CA

QY 1921 AACGGCGACCUAGATCGGC-----TGTGAGCTGCCCCGGGGACACAGGGTGA 1968
 Db 539 AspGlySertypPheGlyLysSerIleLeuAsnIleLysGlySerLysAlaGlyAsn 558
 QY 1969 AAGGCCAATGCGGACGTCGAGGGCCGAGCAGTCAGTCGCTCCGAGCTGCTGCTGAGCTGCT 2028
 Db 559 ArgArgGthralAsnIleLysSerIleGlyLysSerAspLysPheCysLeuSerLysAsp 578
 QY 2029 GGCCTGCGACGACGCCGCTGCGCTGACGCCGAGCTGGCCGCGTCAGGTCGAGCTC 2088
 Db 579 AspIleMetGluIleLeuThrGlyLysProAsp-----AlaYsthrMet 593
 QY 2089 CGACGGGACCTCAGCTACACCCAGGGCTCGAGGTGGACACAGC 2148
 Db 594 LeuGluLysGlyLysGlnIleLeuWetLysAspGlyLeuLeuAspIleAsnIleAla 613
 QY 2149 TCCCTGACGGCGACAACTACCCATATGTCACCGCTCTGCAGAGTGGACACAGC 2199
 Db 614 AsnAlaGlySerAsp-----ProLysAspIleGluGluLysValThr 627

RESULT 15
 S74179
 cyclic nucleotide-gated channel protein - human
 species: Homo sapiens (man)
 C;Species: Homo sapiens (man)
 C;Date: 14-Apr-1998 #sequence_revision 24-Apr-1998 #text_change 16-Jul-1999
 C;Accession: S74179
 R;Yu, W.P.; Grunwald, M.E.; Yau, K.W.
 FEB5 Lett. 393, 211-215, 1996 functional expression and chromosomal localization of a human cyclic nucleotide-gated channel protein
 A;Title: Molecular cloning, functional expression and chromosomal localization of a human cyclic nucleotide-gated channel protein
 A;Reference number: S74179; MURID:9649010; PMID:814292
 A;Accession: S74179
 A;Status: not compared with conceptual translation
 A;Molecule type: mRNA
 A;Residues: 1-695 <DW>
 A;Experimental source: retina
 C;Genetics:
 C;Map position: 2
 A;Superfamily: cyclic nucleotide-gated channel; membrane protein
 C;Keywords: ion channel; ion transport; cyclic nucleotide-binding domain homology <CNA>
 F;482-607/Domain: cAMP receptor protein cyclic nucleotide-binding domain homology <CNA>

Alignment Scores:
 pred. No.: 2.17e-14 Length: 695
 Score: 420.00 Matches: 141
 Percent. Similarity: 42.25% Conservative: 96
 Best Local Similarity: 25.13% Mismatches: 218
 Query Match: 6.90% Indels: 106
 DB: 2 Gaps: 17

US-09-965-830-1_COPY_6_3257 (1-3252) x S74179 (1-695)

QY 787 GRCGTCGACCTGGCCGCGGAGGCTCTTCATCCTGACATGTCGCTGATTTCGCTAC 846
 Db 205 ValLeuAspTyrsSerAlaAspValLeuIrrValLeuAspValLeuValAlaArgThr 224
 QY 847 AGATCGTCGCACTGGCCGAGTGTGTCGCCAAAGCCATTTGCCCACTAC 906
 Db 225 GlyPheIle---GluGlyLysLeuMetValSerAspThrAsnArgLeuIrrPheGlnHistYr 243
 QY 907 --GTCACCAACCTGGTCTCTGCGATGTCATGCGAGGGCTGCCCTTGACCTGCTACAT 963
 Db 244 LysThrIrrThrGlnIlePheLysLeuAspIleSerIleValProThrAspLeuIrr 263
 QY 964 GCCTCAAGGTCAACGTCGACTTGGGCCCACTGCGAGGGCTGGCCCTGCTGCGC 1023
 Db 264 ---LeuLysValGlyThrAsnTyPheGluIleLeuAspIleAsnArgLeuIleLys 280
 QY 1024 CTGGTGCCTGCTGCGGCTGACGCCGACTCTG----- 1059
 Db 281 PheSerArgLeuPheGluIleLeuAspIleAspIleGlyLysGlnIleLeuAsnAsnMet 300
 QY 1060 ---CAGTACAGGCCGTTGGCTCACACTGCTCATGGCGTGTGCTGCCCTGCTCGGCCAC 1116

